Amendments to the Specification

Please insert the attached 9-page Sequence Listing into the application.

Please replace paragraph 12 on pages 3-4 with the following amended paragraph:

[0012] The above and other features and advantages of the present invention will become more apparent by describing in detail exemplary embodiments thereof with reference to the attached drawings in which:

FIG. 1 shows detection of a 43-kDa protein as a PLD2-binding protein;

FIG. 2 shows interaction between actin and PLD2;

FIG. 3A shows the isolation of PLD2-binding protein (p40) by the above blot overlay assay;

FIG. 3B shows the matrix-assisted laser desorption ionization mass spectrum of the digested peptides of p40 (the sequence (SEQ ID NO:8) is provided);

FIG. 4 shows direct interaction between aldolase and PLD2;

FIG. 5 shows detection of a p62 as a PLD2-binding protein;

FIG. 6 shows direct interaction between CRMP-2 and PLD2-PX;

FIG. 7 shows direct interaction between PLC-λ1 and PLD2;

FIG. 8 shows detection of a p35 as a PLD2-binding protein;

FIG. 9 shows direct interaction between Akt and PLD2;

FIG. 10 shows association with PLD1 and GLUT4;

FIG. 11 shows a direct binding of purified PLD1 to the cytoplasmic central loop of GLUT4;

FIGs. 12 and 13 show detection of HSP70 as a PLD2-binding protein;

FIG. 14 shows direct interaction between HSP70 and PLS2;

FIGs. 15A and 15B show detection of dynamin as a PLD-binding protein;

FIG. 16 shows direct interaction between dynamin and PLD2;

FIG. 17 shows detection of munc-18-1 as a PLD-binding protein;

FIG. 18 shows direct interaction between munc-18-1 and PLD2;

FIG. 19 shows detection of p55 protein as a PLD2-binding protein;

FIG. 20 shows that the 55-kDa protein is co-precipitated with PLD2 in COS-7 cells is α- and β-tubulin;

FIG. 21 shows detection of nNOS as a PLD2-binding protein;

FIG. 22 shows interaction between nNOS and PLD2;

FIG. 23 shows direct interaction between integrin beta 3, 5 cytosolic tail and PLD2;

FIG. 24 shows interaction between integrin beta 3 and PLD2;

FIG. 25 shows an interaction between mTOR and PLD2; and

FIGs. 26A, 26B, and 26C show affinity between PLD1 and phosphoinositide-3-phosphate (PIP3) (PLD1, SEQ ID NO:9; p47phox, SEQ ID NO:10; cisk, SEQ ID NO:11; snx1, SEQ ID NO:12; fish, SEQ ID NO:13; p40, SEQ ID NO:14; vas7, SEQ ID NO:15).

Please replace paragraph 81 on page 30 with the following amended paragraph:

[0081] Identification of the 43-kDa protein obtained in the above was performed using peptide mass fingerprinting by matrix-assisted laser desorption ionization/time-of-flight mass spectrometry, according to J. B. Park et al., *J. Biol. Chem.* 275, 21295-21301, 2000. The fraction containing the 43-kDa protein (p43) after co-immunoprecipitation from rat brain extract was separated by 8% SDS-PAGE, and the band corresponding to p43 was excised and digested with trypsin (Roche Molecular Biochemicals) for 6 hours at 37°C. The masses of the tryptic peptides obtained were determined with a Voyager DE time-of-flight mass spectrometer (Perceptive Biosystems, Inc., Farmingham, MA) in the Korea Basic Science Institute (Busan, Korea). The masses obtained, marked as P1-P7, were compared with protein in the Swiss-Protein database using the MS-Fit peptide mass search program. As shown in Table 1, the peptide exhibited molecular masses that were almost identical to the calculated masses of the corresponding theoretically predicted tryptic peptides of β-actin.

Table 1.

Peptide	Sequence[a]	M + H+	
		Observed	Calculated[b]
		Da	
P1	LDLAGR (178-183) (SEQ ID NO:1)	644.36	644.37
P2	ILAPPER (329-335) (SEQ ID NO:2)	795.49	795.47
P3	GYSFTTTAER (197-206) (SEQ ID NO:3)	1132.54	1132.52
P4	HQGVMVGMGQK (40-50) (SEQ ID NO:4)	1187.57	1187.56
P5	QEYDESGPSIVHR (360-372 (SEQ ID NO:5)	1516.72	1516.70
P6	SYELPDGQVITIGNER (239-254) (SEQ ID NO:6)	1790.90	1790.89
P7	VAPEEHPVLLTEAPLNPK (96-113) (SEQ ID NO:7)	1954.03	1954.06

a: the matched peptides cover 21% (81 of 375 amino acids) of the proteins
b: Monoisotopic mass

Please replace paragraph 85 of page 32 with the following amended paragraph:

[0085] The masses of the tryptic peptides so obtained were determined using a Bruker REFLEX reflector time-of-flight mass spectrometer (Bruker-Franzen, Bremen, Germany). Delayed ion extraction resulted in peptide masses in 50 ppm mass accuracy or higher on average. Using the amino acid sequences and the mass numbers of the tryptic peptides of p40, the Swiss-Protein database was searched for a protein match. Fig. 3B (SEQ ID NO:8) shows the matrix-assisted laser desorption ionization mass spectrum of the digested peptides of p40. The masses obtained were compared with protein in the Swiss-Protein database using the MS-Fit peptide mass search program. The peptide exhibited molecular masses that were almost identical to the calculated masses of the corresponding theoretically predicted trytic peptides of aldolase.